GenCore version 4.5

OM protein - protein search, using sw model

Run on: August 21, 2001, 12:06:13 ; Search time 20.59 Seconds
(without alignments)
924.523 Million cell updates/sec

Title: US-09-486-334-2
Perfect score: 1641
Sequence: 1 MATCIDTCRTGNTQDDDSRF.....IPCLTMDQTSYLTEWSDYVI 314

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_0601:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1641	100.0	314	21	AAG45802	Arabidopsis thalia
2	1641	100.0	314	21	AAY93901	Amino acid sequenc
3	1349	82.2	263	21	AAG45803	Arabidopsis thalia
4	1215	74.0	336	21	AAY93903	Amino acid sequenc
5	1215	74.0	391	21	AAY93904	Amino acid sequenc
6	1213	73.9	1772	21	AAG52485	Arabidopsis thalia
7	1213	73.9	1776	21	AAG52484	Arabidopsis thalia
8	1213	73.9	1787	21	AAG52483	Arabidopsis thalia
9	916	55.8	180	21	AAG08083	Arabidopsis thalia
10	880	53.6	286	21	AAY44770	Soybean serine O-a
11	849.5	51.8	312	21	AAG39465	Arabidopsis thalia
12	849.5	51.8	312	21	AAY93902	Amino acid sequenc
13	846.5	51.6	312	21	AAG21076	Arabidopsis thalia
14	846	51.6	294	21	AAY44767	Impatiens balsamia
15	831	50.6	303	21	AAY44768	Rice serine O-acet
16	723.5	44.1	224	21	AAY44769	Rice serine O-acet
17	711	43.3	359	21	AAY93905	Amino acid sequenc
18	656	40.0	157	21	AAY44771	Soybean serine O-a
19	652.5	39.8	273	18	AAW35073	E. coli serine ace
20	648.5	39.5	258	18	AAW35084	E. coli serine ace
21	648.5	39.5	259	18	AAW35083	E. coli serine ace
22	648.5	39.5	263	18	AAW35094	E. coli serine ace
23	648.5	39.5	268	18	AAW35093	E. coli serine ace
24	648.5	39.5	270	18	AAW35092	E. coli serine ace
25	648.5	39.5	271	18	AAW35091	E. coli serine ace
26	648.5	39.5	273	13	AAR37580	E.coli serine tran
27	648.5	39.5	273	18	AAW35074	E. coli serine ace
28	648.5	39.5	273	18	AAW16618	Wild type Escheric
29	648.5	39.5	273	20	AAY23827	Protein encoded by
30	648.5	39.5	273	21	AAY57823	Escherichia coli s
31	646.5	39.4	273	18	AAW35070	E. coli serine ace
32	645.5	39.3	273	18	AAW35078	E. coli serine ace
33	645	39.3	253	21	AAY57826	Escherichia coli s
34	644	39.2	253	21	AAY57827	Escherichia coli s
35	643.5	39.2	257	18	AAW35085	E. coli serine ace
36	643.5	39.2	273	18	AAW35075	E. coli serine ace
37	643.5	39.2	273	18	AAW35077	E. coli serine ace
38	642.5	39.2	273	18	AAW35071	E. coli serine ace
39	642.5	39.2	273	18	AAW35068	E. coli serine ace
40	642	39.1	129	21	AAG08084	Arabidopsis thalia
41	642	39.1	253	21	AAY57830	Escherichia coli s
42	641.5	39.1	273	18	AAW35082	E. coli serine ace
43	641.5	39.1	273	18	AAW35069	E. coli serine ace
44	641	39.1	253	21	AAY57831	Escherichia coli s
45	640.5	39.0	175	21	AAY44765	Corn serine O-acet

ALIGNMENTS

RESULT 1
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ID AAG45802 standard; Protein; 314 AA.
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AC AAG45802;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 57548.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
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Db     301 dqtsyltewsdyvi 314
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RESULT 2
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ID AAY93901 standard; Protein; 314 AA.
XX
AC AAY93901;
XX
DT 03-OCT-2000 (first entry)
XX
DE Amino acid sequence of serine acetyltransferase (SAT) isoform SAT3.
XX
KW Serine acetyltransferase; SAT; SAT3; transgenic plant; cysteine;
KW glutathione; methionine; nutrient value; plant-derived food;
KW glutathione; viral resistance.
XX
OS Arabidopsis thaliana.
XX
PN WO200036127-A1.
XX
PD 22-JUN-2000.
XX
PF 17-DEC-1999; 99WO-FR03179.
XX
PR 17-DEC-1998; 98FR-0016163.
XX
PA (AVET) AVENTIS CROPSCIENCE SA.
XX
PI Droux M, Lappartient A, Derose R, Job D;
XX
DR WPI; 2000-431603/37.
DR N-PSDB; AAA47173.
XX
PT Increasing production of sulfur-containing compounds, e.g. cysteine or
PT methionine, in plants, useful e.g. for improving nutritional value, by
PT overexpressing serine acetyltransferase -
XX
PS Claim 9; Page 50-51; 69pp; French.
XX
CC The present sequence represents an isoform of serine acetyltransferase
CC (SAT). The SAT polynucleotide is used to produce transgenic plants,
CC which have increased production of cysteine, glutathione, methionine
CC and their sulfur-containing derivatives. SAT catalyses conversion of
CC serine to O-acetylserine which is a precursor (by reaction with sulphide)
CC for cysteine, itself a precursor for the other sulphur-containing
CC compounds. The SAT polynucleotides and polypeptides are used to improve
CC the nutrient value of plant-derived foods, and also (associated with
CC increased production of glutathione) to improve resistance to stress.
XX
SQ Sequence 314 AA;

Query Match 100.0%; Score 1641; DB 21; Length 314;
Best Local Similarity 100.0%; Pred. No. 2e-151;
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      61 KQEPILSNYYYASITSHRSLESALAHILSVKLSNLNLPSNTLFELFISVLEESPEIIEST 120
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Qy     241 IGAGSCILGNITIGEGAKIGSGSVVVKDVPARTTAVGNPARLIGGKENPRKHDKIPCLTM 300
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Db     241 igagscilgnitigegakigsgsvvvkdvparttavgnparliggkenprkhdkipcltm 300

Qy     301 DQTSYLTEWSDYVI 314
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RESULT 3
AAG45803
ID AAG45803 standard; Protein; 263 AA.
XX
AC AAG45803;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 57549.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.

XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
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PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
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PR   12-OCT-1999;   99US-0158369.
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PR   25-OCT-1999;   99US-0161406.
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PR   26-OCT-1999;   99US-0161361.
PR   28-OCT-1999;   99US-0161920.
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PR   28-OCT-1999;   99US-0161993.
PR   29-OCT-1999;   99US-0162142.

  Query Match             82.2%;  Score 1349;  DB 21;  Length 263;
  Best Local Similarity   100.0%;  Pred. No. 4e-123;
  Matches  263;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      52 MLEEAKSDVKQEPILSNYYYASITSHRSLESALAHILSVKLSNLNLPSNTLFELFISVLE 111
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 mleeaksdvkqepilsnyyyasitshrslesalahilsvklsnlnlpsntlfelfisvle 60

Qy     112 ESPEIIESTKQDLIAVKERDPACISYVHCFLGFKGFLACQAHRIAHTLWKQNRKIVALLI 171
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 espeiiestkqdliavkerdpacisyvhcflgfkgflacqahriahtlwkqnrkivalli 120

Qy     172 QNRVSESFAVDIHPGAKIGKGILLDHATGVVIGETAVVGDNVSILHGVTLGGTGKQSGDR 231
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 qnrvsesfavdihpgakigkgilldhatgvvigetavvgdnvsilhgvtlggtgkqsgdr 180

Qy     232 HPKIGDGVLIGAGSCILGNITIGEGAKIGSGSVVVKDVPARTTAVGNPARLIGGKENPRK 291
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 hpkigdgvligagscilgnitigegakigsgsvvvkdvparttavgnparliggkenprk 240

Qy     292 HDKIPCLTMDQTSYLTEWSDYVI 314
           |||||||||||||||||||||||
Db     241 hdkipcltmdqtsyltewsdyvi 263


RESULT   4
AAY93903
ID   AAY93903 standard; Protein; 336 AA.
XX
AC   AAY93903;
XX
DT   03-OCT-2000  (first entry)
XX
DE   Amino acid sequence of serine acetyltransferase (SAT) isoform SAT1'.
XX
KW   Serine acetyltransferase; SAT; SAT1'; transgenic plant; cysteine;
KW   glutathione; methionine; nutrient value; plant-derived food;
KW   glutathione; viral resistance.
XX
OS   Arabidopsis thaliana.
XX
PN   WO200036127-A1.
XX
PD   22-JUN-2000.
XX
PF   17-DEC-1999;   99WO-FR03179.
XX
PR   17-DEC-1998;   98FR-0016163.
XX
PA   (AVET ) AVENTIS CROPSCIENCE SA.
XX
PI   Droux M,  Lappartient A,  Derose R,  Job D;
XX
DR   WPI; 2000-431603/37.
DR   N-PSDB; AAA47175.
XX
PT   Increasing production of sulfur-containing compounds, e.g. cysteine or
PT   methionine, in plants, useful e.g. for improving nutritional value, by
PT   overexpressing serine acetyltransferase
XX
PS   Claim 14; Page 53-54; 69pp; French.
XX
CC   The present sequence represents an isoform of serine acetyltransferase
CC   (SAT). The SAT polynucleotide is used to produce transgenic plants,
CC   which have increased production of cysteine, glutathione, methionine
CC   and their sulfur-containing derivatives. SAT catalyses conversion of
CC   serine to O-acetylserine which is a precursor (by reaction with sulphide)
CC   for cysteine, itself a precursor for the other sulphur-containing
CC   compounds. The SAT polynucleotides and polypeptides are used to improve
CC   the nutrient value of plant-derived foods, and also (associated with
CC   increased production of glutathione) to improve resistance to stress.
XX
SQ   Sequence   336 AA;

  Query Match             74.0%;  Score 1215;  DB 21;  Length 336;
  Best Local Similarity   72.0%;  Pred. No. 6.2e-110;
  Matches  242;  Conservative   31;  Mismatches   41;  Indels   22;  Gaps    4;

Qy       1 MATCIDTCRTGNTQ----------DDDSRFCCIKNFFRPGFS----VNRKIHHTQ--IED 44
           || ||||||||  |           ||:| |  :  |  |  |        |  ||:  :||
Db       1 maacidtcrtgkpqisprdsskhhddesgfrymnyfrypdrssfngtqtktlhtrplled 60

Qy      45 ------DDDVWIKMLEEAKSDVKQEPILSNYYYASITSHRSLESALAHILSVKLSNLNLP 98
                 |||| |: ||||||: :||||:| ||:||| | ||||:|||: ||||||||||
Db      61 ldrdaevddvwakireeaksdiakepivsayyhasivsqrsleaalantlsvklsnlnlp 120

Qy      99 SNTLFELFISVLEESPEIIESTKQDLIAVKERDPACISYVHCFLGFKGFLACQAHRIAHT 158
           |||||:||  ||: :|:|:|| | ||:||||||||||||||||| ||||||||||||||
Db     121 sntlfdlfsgvlqgnpdivesvkldllavkerdpacisyvhcflhfkgflacqahriahe 180

Qy     159 LWKQNRKIVALLIQNRVSESFAVDIHPGAKIGKGILLDHATGVVIGETAVVGDNVSILHG 218
           || |:|||:||||||||||:|||| ||||||| |||||||| :|||||||||:||||||
Db     181 lwtqdrkilalliqnrvseafavdfhpgakigtgilldhataivigetavvgnnvsilhn 240

Qy     219 VTLGGTGKQSGDRHPKIGDGVLIGAGSCILGNITIGEGAKIGSGSVVVKDVPARTTAVGN 278
           ||||||||| |||||||||||||||:|||||||||||||||:||||:|||| |||||||
Db     241 vtlggtgkqcgdrhpkigdgvligagtcilgnitigegakigagsvvlkdvpprttavgn 300

Qy     279 PARLIGGKENPRKHDKIPCLTMDQTSYLTEWSDYVI 314
           ||||:|||:||: ||||| |||||||:::||||||||
Db     301 parllggkdnpkthdkipgltmdqtshisewsdyvi 336
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RESULT   5
AAY93904
ID   AAY93904 standard; Protein; 391 AA.
XX
AC   AAY93904;
XX
DT   03-OCT-2000  (first entry)
XX
DE   Amino acid sequence of serine acetyltransferase (SAT) isoform SAT1.
XX
KW   Serine acetyltransferase; SAT; SAT1; transgenic plant; cysteine;
KW   glutathione; methionine; nutrient value; plant-derived food;
KW   glutathione; viral resistance.
XX
OS   Arabidopsis thaliana.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..63
FT                   /note= "signal peptide"
XX
PN   WO200036127-A1.
XX
PD   22-JUN-2000.
XX
PF   17-DEC-1999;   99WO-FR03179.
XX
PR   17-DEC-1998;   98FR-0016163.
XX
PA   (AVET ) AVENTIS CROPSCIENCE SA.
XX
PI   Droux M,  Lappartient A,  Derose R,  Job D;
XX
DR   WPI; 2000-431603/37.
DR   N-PSDB; AAA47176.
XX
PT   Increasing production of sulfur-containing compounds, e.g. cysteine or
PT   methionine, in plants, useful e.g. for improving nutritional value, by
PT   overexpressing serine acetyltransferase  -
XX
PS   Disclosure; Page 54-56; 69pp; French.
XX
CC   The present sequence represents an isoform of serine acetyltransferase
CC   (SAT). The SAT polynucleotide is used to produce transgenic plants,
CC   which have increased production of cysteine, glutathione, methionine
CC   and their sulfur-containing derivatives. SAT catalyses conversion of
CC   serine to O-acetylserine which is a precursor (by reaction with sulphide)
CC   for cysteine, itself a precursor for the other sulphur-containing
CC   compounds. The SAT polynucleotides and polypeptides are used to improve
CC   the nutrient value of plant-derived foods, and also (associated with
CC   increased production of glutathione) to improve resistance to stress.
XX
SQ   Sequence   391 AA;


  Query Match             74.0%;  Score 1215;  DB 21;  Length 391;
  Best Local Similarity   72.0%;  Pred. No. 7.7e-110;
  Matches  242;  Conservative   31;  Mismatches   41;  Indels   22;  Gaps    4;

Qy       1 MATCIDTCRTGNTQ----------DDDSRFCCIKNFFRPGFS----VNRKIHHTQ--IED 44
           || ||||||||  |           ||:| |  :  |  |  |       |  ||:  :||
Db      56 maacidtcrtgkpqisprdsskhhddesgfrymnyfrypdrssfngtqtktlhtrplled 115

Qy      45 ------DDDVWIKMLEEAKSDVKQEPILSNYYYASITSHRSLESALAHILSVKLSNLNLP 98
                 |||| |: |||||: :|||:| ||:||| | ||||:|||: ||||||||||
Db     116 ldrdaevddvwakireeaksdiakepivsayyhasivsqrsleaalantlsvklsnlnlp 175

Qy      99 SNTLFELFISVLEESPEIIESTKQDLIAVKERDPACISYVHCFLGFKGFLACQAHRIAHT 158
           |||||:||  ||: :|:|:|| | ||:|||||||||||||||| ||||||||||||||
Db     176 sntlfdlfsgvlqgnpdivesvkldllavkerdpacisyvhcflhfkgflacqahriahe 235

Qy     159 LWKQNRKIVALLIQNRVSESFAVDIHPGAKIGKGILLDHATGVVIGETAVVGDNVSILHG 218
           || |:|||:|||||||||:|||| ||||||| |||||||| :|||||||||:||||||
Db     236 lwtqdrkilalliqnrvseafavdfhpgakigtgilldhataivigetavvgnnvsilhn 295

Qy     219 VTLGGTGKQSGDRHPKIGDGVLIGAGSCILGNITIGEGAKIGSGSVVVKDVPARTTAVGN 278
           |||||||| |||||||||||||||:|||||||||||||||:||||:|||| |||||||
Db     296 vtlggtgkqcgdrhpkigdgvligagtcilgnitigegakigagsvvlkdvpprttavgn 355

Qy     279 PARLIGGKENPRKHDKIPCLTMDQTSYLTEWSDYVI 314
           ||||:|||:||: ||||| |||||||:::|||||||
Db     356 parllggkdnpkthdkipgltmdqtshisewsdyvi 391


RESULT   6
AAG52485
ID   AAG52485 standard; Protein; 1772 AA.
XX
AC   AAG52485;
XX
DT   18-OCT-2000  (first entry)
XX
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 66722.
XX
KW   Protein identification; signal transduction pathway; metabolic pathway;
KW   hybridisation assay; genetic mapping; gene expression control; promoter;
KW   termination sequence.
XX
OS   Arabidopsis thaliana.
XX
PN   EP1033405-A2.
XX
PD   06-SEP-2000.
XX
PF   25-FEB-2000; 2000EP-0301439.
XX
PR   25-FEB-1999;   99US-0121825.
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PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
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PR 29-OCT-1999; 99US-0162142.

Query Match 73.9%; Score 1213; DB 21; Length 1772;
Best Local Similarity 71.4%; Pred. No. 1.1e-108;
Matches 240; Conservative 33; Mismatches 41; Indels 22; Gaps 4;

Qy 1 MATCIDTCRTGNTQ----------DDDSRFCCIKNFFRPGFS----VNRKIHHTQ--IED 44

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Qy     219 VTLGGTGKQSGDRHPKIGDGVLIGAGSCILGNITIGEGAKIGSGSVVVKDVPARTTAVGN 278
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Qy     279 PARLIGGKENPRKHDKIPCLTMDQTSYLTEWSDYVI 314
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DT   18-OCT-2000  (first entry)
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DE   Arabidopsis thaliana protein fragment SEQ ID NO: 66721.
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KW   Protein identification; signal transduction pathway; metabolic pathway;
KW   hybridisation assay; genetic mapping; gene expression control; promoter;
KW   termination sequence.
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Query Match 73.9%; Score 1213; DB 21; Length 1776;
Best Local Similarity 71.4%; Pred. No. 1.1e-108;
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XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
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PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 73.9%; Score 1213; DB 21; Length 1787;
Best Local Similarity 71.4%; Pred. No. 1.1e-108;
Matches 240; Conservative 33; Mismatches 41; Indels 22; Gaps 4;

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Qy       1 MATCIDTCRTGNTQ----------DDDSRFCCIKNFFRPGFS----VNRKIHHTQ--IED 44
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Db      56 maacidtcrtgkpqisprdsskhhddesgfrymnyfrypdrssfngtqtktlhtrplled 115

Qy      45 ------DDDVWIKMLEEAKSDVKQEPILSNYYYASITSHRSLESALAHILSVKLSNLNLP 98
                 |||| |: |||||: :|||:| ||:||| | ||||:|||: ||||||||||
Db     116 ldrdaevddvwakireeaksdiakepivsayyhasivsqrsleaalantlsvklsnlnlp 175

Qy      99 SNTLFELFISVLEESPEIIESTKQDLIAVKERDPACISYVHCFLGFKGFLACQAHRIAHT 158
           |||||:||  ||: :|:|:|| | ||:||||||||||||||| ||||||||||||
Db     176 sntlfdlfsgvlqgnpdivesvkldllavkerdpacisyvhcflhfkgflacqahriahe 235

Qy     159 LWKQNRKIVALLIQNRVSESFAVDIHPGAKIGKGILLDHATGVVIGETAVVGDNVSILHG 218
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Db     236 lwtqdrkilalliqnrvseafavdfhpgakigtgilldhataivigetavvgnnvsilhn 295

Qy     219 VTLGGTGKQSGDRHPKIGDGVLIGAGSCILGNITIGEGAKIGSGSVVVKDVPARTTAVGN 278
           |||||||||| ||||||||||||||||:|||||||||||||||:||||:|||| |||||||
Db     296 vtlggtgkqcgdrhpkigdgvligagtcilgnitigegakigagsvvlkdvpprttavgn 355

Qy     279 PARLIGGKENPRKHDKIPCLTMDQTSYLTEWSDYVI 314
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RESULT 9
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ID AAG08083 standard; Protein; 180 AA.
XX
AC AAG08083;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 5483.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
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PR   28-OCT-1999;   99US-0161993.
PR   29-OCT-1999;   99US-0162142.

  Query Match             55.8%;  Score 916;  DB 21;  Length 180;
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Db      61 kqepilsnyyyasitshrslesalahilsvklsnlnlpsntlfelfisvleespeiiest 120

Qy     121 KQDLIAVKERDPACISYVHCFLGFKGFLACQAHRIAHTLWKQNRKIVALLIQNRVSESFA 180
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Db     121 kqdliavkerdpacisyvhcflgfkgflacqahriahtlwkqnrkivalliqnrvsesfa 180


RESULT  10
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ID   AAY44770 standard; Protein; 286 AA.
XX
AC   AAY44770;
XX
DT   04-MAY-2000  (first entry)
XX
DE   Soybean serine O-acetyltransferase-1.
XX
KW   Serine O-acetyltransferase; sulphate assimilation; O-acetylserine;
KW   soybean; clone sr1.pk0162.a9; cysteine formation; marker; probe;
KW   plant breeding; transgenic plant.
XX
OS   Glycine max.
XX
PN   WO200004167-A2.
XX
PD   27-JAN-2000.
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PF   13-JUL-1999;   99WO-US15872.
XX
PR   14-JUL-1998;   98US-0092833.
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XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Falco SC, Allen SM, Maxwell CA;
XX
DR WPI; 2000-182432/16.
DR N-PSDB; AAZ50087.
XX
PT New isolated nucleic acid fragment encoding a sulfate assimilation
PT protein in plants, useful as probes to isolate genes encoding
PT homologous proteins from other plant species -
XX
PS Claim 6; Page 38-39; 44pp; English.
XX
CC The present sequence is the serine O-acetyltransferase, a sulphate
CC assimilation protein isolated from soybean. This is obtained from srl
CC cDNA library, from clone srl.pk0162.a9, derived from soybean root
CC library. It has 87% sequence identity to Citrullus lanatus serine
CC O-acetyltransferase. Serine O-acetyltransferase converts serine
CC to O-acetylserine, that is involved in the formation of cysteine.
CC This sequence is used as a probe to isolate other plant sulphate
CC assimilation proteins, for genetic and physical mapping of related genes
CC and as markers of traits linked to the gene. This is useful for plant
CC breeding. It is also used to create transgenic plants with altered
CC levels of serine O-acetyltransferase, or found in cell types or
CC developmental stages in which they are not normally found.
XX
SQ Sequence 286 AA;

Query Match 53.6%; Score 880; DB 21; Length 286;
Best Local Similarity 59.6%; Pred. No. 1.9e-77;
Matches 162; Conservative 49; Mismatches 61; Indels 0; Gaps 0;

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Db      15 deegwvwgqikaearrdaesepalasylystilshsslersisfhlgnklcsstllstll 74

Qy     103 FELFISVLEESPEIIESTKQDLIAVKERDPACISYVHCFLGFKGFLACQAHRIAHTLWKQ 162
           ::||::     | :  :   || | :|||||:|| || | :|||||||||:|| ||:|
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Qy     163 NRKIVALLIQNRVSESFAVDIHPGAKIGKGILLDHATGVVIGETAVVGDNVSILHGVTLG 222
           :|: :|| : :|::: ||||||| |:|||||| ||||||: ||| :|:|||||| ||||
Db     135 srrplalalhsriadvfavdihpparigkgilfdhatgvvvretasignnvsilhhvtlg 194

Qy     223 GTGKQSGDRHPKIGDGVLIGAGSCILGNITIGEGAKIGSGSVVVKDVPARTTAVGNPARL 282
           ||||  |||||||||||||||: ||||| ||||||:|:||||: ||| ||||||||||
Db     195 gtgkvggdrhpkigdgvligagatilgnikigegakvgagsvvlidvpprttavgnparl 254

Qy     283 IGGKENPRKHDKIPCLTMDQTSYLTEWSDYVI 314
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Db     255 vggkekpskhedvpgesmdhtsfisewsdyii 286
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RESULT 11
AAG39465
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AC AAG39465;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48833.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-0301439.
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PR 05-MAR-1999; 99US-0123180.
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PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
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PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
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PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
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PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
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PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 51.8%; Score 849.5; DB 21; Length 312;
Best Local Similarity 59.7%; Pred. No. 2.1e-74;
Matches 160; Conservative 45; Mismatches 62; Indels 1; Gaps 1;

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Qy     48 VWIKMLEEAKSDVKQEPILSNYYYASITSHRSLESALAHILSVKLSNLNLPSNTLFELFI 107
          :| ::  ||: | : || |::| |::| || ||| :::  |  || :  | |  |::||:
Db     45 lwtqikaearrdaeaepalasylystilshsslersisfhlgnklcsstllstllydlfl 104

Qy    108 SVLEESPEIIESTKQDLIAVKERDPACISYVHCFLGFKGFLACQAHRIAHTLWKQNRKIV 167
          :     | :  :|  || | : |||||||: || | :||||| ||||::| || |:|| :
Db    105 ntfssdpslrnatvadlraarvrdpacisfshcllnykgflaiqahrvshklwtqsrkpl 164

Qy    168 ALLIQNRVSESFAVDIHPGAKIGKGILLDHATGVVIGETAVVGDNVSILHGVTLGGTGKQ 227
          || : :|:|: ||||||| ||||||||||||||||:|||||:|:|||||| ||||||||
Db    165 alalhsrisdvfavdihpaakigkgilldhatgvvvgetavignnvsilhhvtlggtgka 224

Qy    228 SGDRHPKIGDGVLIGAGSCILGNITIGEGAKIGSGSVVVKDVPARTTAVGNPARLIGGKE 287
           ||||||||| ||||: |||| || |||:|:|||| ||| | ||||||||:||||
Db    225 cgdrhpkigdgcligagatilgnvkigagakvgagsvvlidvpcrgtavgnparlvggke 284

Qy    288 NPRKHD-KIPCLTMDQTSYLTEWSDYVI 314
           |  || : |  :|| ||:::|||||:|
Db    285 kptihdeecpgesmdhtsfisewsdyii 312
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RESULT 12
AAY93902
ID AAY93902 standard; Protein; 312 AA.
XX
AC AAY93902;
XX
DT 03-OCT-2000 (first entry)
XX
DE Amino acid sequence of serine acetyltransferase (SAT) isoform SAT3'.

```
XX
KW   Serine acetyltransferase; SAT; SAT3'; transgenic plant; cysteine;
KW   glutathione; methionine; nutrient value; plant-derived food;
KW   glutathione; viral resistance.
XX
OS   Arabidopsis thaliana.
XX
PN   WO200036127-A1.
XX
PD   22-JUN-2000.
XX
PF   17-DEC-1999;   99WO-FR03179.
XX
PR   17-DEC-1998;   98FR-0016163.
XX
PA   (AVET ) AVENTIS CROPSCIENCE SA.
XX
PI   Droux M,  Lappartient A,  Derose R,  Job D;
XX
DR   WPI; 2000-431603/37.
DR   N-PSDB; AAA47174.
XX
PT   Increasing production of sulfur-containing compounds, e.g. cysteine or
PT   methionine, in plants, useful e.g. for improving nutritional value, by
PT   overexpressing serine acetyltransferase -
XX
PS   Claim 11; Page 51-53; 69pp; French.
XX
CC   The present sequence represents an isoform of serine acetyltransferase
CC   (SAT). The SAT polynucleotide is used to produce transgenic plants,
CC   which have increased production of cysteine, glutathione, methionine
CC   and their sulfur-containing derivatives. SAT catalyses conversion of
CC   serine to O-acetylserine which is a precursor (by reaction with sulphide)
CC   for cysteine, itself a precursor for the other sulphur-containing
CC   compounds. The SAT polynucleotides and polypeptides are used to improve
CC   the nutrient value of plant-derived foods, and also (associated with
CC   increased production of glutathione) to improve resistance to stress.
XX
SQ   Sequence   312 AA;


  Query Match             51.8%;  Score 849.5;  DB 21;  Length 312;
  Best Local Similarity   59.7%;  Pred. No. 2.1e-74;
  Matches  160;  Conservative   45;  Mismatches   62;  Indels    1;  Gaps    1;

Qy      48 VWIKMLEEAKSDVKQEPILSNYYYASITSHRSLESALAHILSVKLSNLNLPSNTLFELFI 107
           :| ::  ||: | : || |::| |::| || ||| :::  |  || :  | |  |::||:
Db      45 lwtqikaearrdaeaepalasylystilshsslersisfhlgnklcsstllstllydlfl 104

Qy     108 SVLEESPEIIESTKQDLIAVKERDPACISYVHCFLGFKGFLACQAHRIAHTLWKQNRKIV 167
           :     | :  :|  || | : |||||||: || | :||||| ||||::| || |:|| :
Db     105 ntfssdpslrnatvadlraarvrdpacisfshcllnykgflaiqahrvshklwtqsrkpl 164

Qy     168 ALLIQNRVSESFAVDIHPGAKIGKGILLDHATGVVIGETAVVGDNVSILHGVTLGGTGKQ 227
           || : :|:|: ||||||| ||||||||||||||||:|||||:|:|||||| ||||||||
Db     165 alalhsrisdvfavdihpaakigkgilldhatgvvvgetavignnvsilhhvtlggtgka 224

Qy     228 SGDRHPKIGDGVLIGAGSCILGNITIGEGAKIGSGSVVVKDVPARTTAVGNPARLIGGKE 287
           |||||||||| |||||: |||||: || |||:|:|||||: ||| | ||||||||:||||
Db     225 cgdrhpkigdgcligagatilgnvkigagakvgagsvvlidvpcrgtavgnparlvggke 284

Qy     288 NPRKHD-KIPCLTMDQTSYLTEWSDYVI 314
           |  || : |  :|| ||:::|||||:|
Db     285 kptihdeecpgesmdhtsfisewsdyii 312


RESULT  13
AAG21076
ID   AAG21076 standard; Protein; 312 AA.
XX
AC   AAG21076;
XX
DT   17-OCT-2000  (first entry)

XX
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 23500.
XX
KW   Protein identification; signal transduction pathway; metabolic pathway;
KW   hybridisation assay; genetic mapping; gene expression control; promoter;
KW   termination sequence.
XX
OS   Arabidopsis thaliana.
XX
PN   EP1033405-A2.
XX
PD   06-SEP-2000.
XX
PF   25-FEB-2000; 2000EP-0301439.
XX
PR   25-FEB-1999;   99US-0121825.
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PR   09-MAR-1999;   99US-0123548.
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PR   25-MAR-1999;   99US-0126264.
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PR   01-APR-1999;   99US-0127462.
PR   06-APR-1999;   99US-0128234.
PR   08-APR-1999;   99US-0128714.
PR   16-APR-1999;   99US-0129845.
PR   19-APR-1999;   99US-0130077.
PR   21-APR-1999;   99US-0130449.
PR   23-APR-1999;   99US-0130510.
PR   23-APR-1999;   99US-0130891.
PR   28-APR-1999;   99US-0131449.
PR   30-APR-1999;   99US-0132048.
PR   30-APR-1999;   99US-0132407.
PR   04-MAY-1999;   99US-0132484.
PR   05-MAY-1999;   99US-0132485.
PR   06-MAY-1999;   99US-0132486.
PR   06-MAY-1999;   99US-0132487.
PR   07-MAY-1999;   99US-0132863.
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PR   14-MAY-1999;   99US-0134218.
PR   14-MAY-1999;   99US-0134219.
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PR   14-MAY-1999;   99US-0134370.
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PR   28-MAY-1999;   99US-0136782.
PR   01-JUN-1999;   99US-0137222.
PR   03-JUN-1999;   99US-0137528.
PR   04-JUN-1999;   99US-0137502.
PR   07-JUN-1999;   99US-0137724.
PR   08-JUN-1999;   99US-0138094.
PR   10-JUN-1999;   99US-0138540.
PR   10-JUN-1999;   99US-0138847.
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PR   18-JUN-1999;   99US-0139455.
PR   18-JUN-1999;   99US-0139456.
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PR   18-JUN-1999;   99US-0139763.
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PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
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PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
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PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
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PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
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PR 14-OCT-1999; 99US-0159637.
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PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 51.6%; Score 846.5; DB 21; Length 312;
Best Local Similarity 59.7%; Pred. No. 4e-74;
Matches 160; Conservative 44; Mismatches 63; Indels 1; Gaps 1;

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Qy      48 VWIKMLEEAKSDVKQEPILSNYYYASITSHRSLESALAHILSVKLSNLNLPSNTLFELFI 107
           :| ::  ||: | : || |::| |::| || ||| :::  |  || :  | |  |::||:
Db      45 lwtqikaearrdaeaepalasylystilshsslersisfhlgnklcsstllstllydlfl 104

Qy     108 SVLEESPEIIESTKQDLIAVKERDPACISYVHCFLGFKGFLACQAHRIAHTLWKQNRKIV 167
           :    | :  :|  || |   |||||||: || | :||||| ||||::| || |:|| :
Db     105 ntfssdpslrnatvadlraaxvrdpacisfshcllnykgflaiqahrvshklwtqsrkpl 164

Qy     168 ALLIQNRVSESFAVDIHPGAKIGKGILLDHATGVVIGETAVVGDNVSILHGVTLGGTGKQ 227
           || : :|:|: ||||||| |||||||||||||||:|||||:|:|||||| ||||||||
Db     165 alalhsrisdvfavdihpaakigkgilldhatgvvvgetavignnvsilhhvtlggtgka 224

Qy     228 SGDRHPKIGDGVLIGAGSCILGNITIGEGAKIGSGSVVVKDVPARTTAVGNPARLIGGKE 287
           |||||||||| ||||: |||: || |||:|:|||: ||| | |||||||||:||||
Db     225 cgdrhpkigdgcligagatilgnvkigagakvgagsvvlidvpcrgtavgnparlvggke 284

Qy     288 NPRKHD-KIPCLTMDQTSYLTEWSDYVI 314
           |  || : |  :|| ||:::|||||:|
Db     285 kptihdeecpgesmdhtsfisewsdyii 312
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RESULT  14
AAY44767
ID   AAY44767 standard; Protein; 294 AA.
XX
AC   AAY44767;
XX
DT   04-MAY-2000  (first entry)
XX
DE   Impatiens balsamia serine O-acetyltransferase.
XX
KW   Serine O-acetyltransferase; sulphate assimilation; clone ids.pk0030.b6;
KW   O-acetylserine; cysteine formation; marker; probe; plant breeding;
KW   transgenic plant.
XX
OS   Impatiens balsamia.
XX
PN   WO200004167-A2.
XX
PD   27-JAN-2000.
XX
PF   13-JUL-1999;   99WO-US15872.
XX
PR   14-JUL-1998;   98US-0092833.
XX
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI   Falco SC,  Allen SM,  Maxwell CA;
XX
DR   WPI; 2000-182432/16.
DR   N-PSDB; AAZ50084.
XX
PT   New isolated nucleic acid fragment encoding a sulfate assimilation
PT   protein in plants, useful as probes to isolate genes encoding
PT   homologous proteins from other plant species -
XX
PS   Claim 6; Page 34; 44pp; English.
XX
CC   The present amino acid sequence is the serine O-acetyltransferase, a
CC   sulphate assimilation protein from Impatiens balsamia. This is obtained
CC   from clone ids.pk0030.b6, derived from I. balsamia developing seed,
CC   ids cDNA library. It has 80% identity to Citrullus lanatus serine
CC   O-acetyltransferase. Serine O-acetyltransferase converts serine
CC   to O-acetylserine, that is involved in the formation of cysteine.
CC   This sequence is used as a probe to isolate other plant sulphate
CC   assimilation proteins, for genetic and physical mapping of related genes
CC   and as markers of traits linked to the gene. This is useful for plant
CC   breeding. It is also used to create transgenic plants with altered
CC   levels of serine O-acetyltransferase, or found in cell types or
CC   developmental stages in which they are not normally found.
XX
SQ   Sequence   294 AA;
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  Query Match           51.6%;  Score 846;  DB 21;  Length 294;
  Best Local Similarity   57.8%;  Pred. No. 4.1e-74;
  Matches  159;  Conservative   51;  Mismatches   63;  Indels    2;  Gaps    1;

Qy      42 IEDDDD--VWIKMLEEAKSDVKQEPILSNYYYASITSHRSLESALAHILSVKLSNLNLPS 99
           :|| ::  || ::  ||: | : || |::| |::| || || ::|:  |  || :  | |
Db      20 vedaeesgvwsqikaearrdaesepalasylystilshsslaaslsfhlgnklcsstlls 79

Qy     100 NTLFELFISVLEESPEIIESTKQDLIAVKERDPACISYVHCFLGFKGFLACQAHRIAHTL 159
             |::||: ||     :  :   || | ::||||| |: || | :|||| || |:|| :
Db      80 tllydlflgvlssdaslraaavadlraarqrdpactsfshcllnykgflaiqaqrvahkm 139

Qy     160 WKQNRKIVALLIQNRVSESFAVDIHPGAKIGKGILLDHATGVVIGETAVVGDNVSILHGV 219
           | |||| ::| :|:|::: |:|||| |:||||:||||||||||||||:|:|||||| |
Db     140 wsqnrkplslalqsriadvfsvdihpaarigkgvlldhatgvvigetavignnvsilhhv 199

Qy     220 TLGGTGKQSGDRHPKIGDGVLIGAGSCILGNITIGEGAKIGSGSVVVKDVPARTTAVGNP 279
           |||||||| |||||||||||||||: |||| |||||||:||:|: |||  |||||||
Db     200 tlggtgkqggdrhpkigdgvligagatilgnvrigegakigagslvlidvppwttavgnp 259

Qy     280 ARLIGGKENPRKHDKIPCLTMDQTSYLTEWSDYVI 314
           |||:|||: |  |  :|  :|| ||::: |||:||
Db     260 arlvggkdkpnvhadvpgesmdhtsfislwsdfvi 294
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RESULT  15
AAY44768
ID   AAY44768 standard; Protein; 303 AA.
XX
AC   AAY44768;
XX
DT   04-MAY-2000  (first entry)
XX
DE   Rice serine O-acetyltransferase-1.
XX
KW   Serine O-acetyltransferase; sulphate assimilation; O-acetylserine;
KW   rice; clone rlr24.pk0069.a11; cysteine formation; marker; probe;
KW   plant breeding; transgenic plant.
XX
OS   Oryza sativa.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 26
FT                   /note= "Encoded by GCG"
XX
PN   WO200004167-A2.
XX
PD   27-JAN-2000.
XX
PF   13-JUL-1999;   99WO-US15872.
XX
PR   14-JUL-1998;   98US-0092833.
XX
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI   Falco SC,  Allen SM,  Maxwell CA;
XX
DR   WPI; 2000-182432/16.
DR   N-PSDB; AAZ50085.
XX
PT   New isolated nucleic acid fragment encoding a sulfate assimilation
PT   protein in plants, useful as probes to isolate genes encoding
PT   homologous proteins from other plant species -
XX
PS   Claim 6; Page 35-36; 44pp; English.
XX
CC   The present sequence is the rice serine O-acetyltransferase, a sulphate
CC   assimilation protein. This is obtained from rlr24 cDNA library, clone
CC   rlr24.pk0069.a11, derived from rice leaf infected with Magaporthe grisea
CC   strain 4360-R-62. It has 72% sequence identity to Citrullus lanatus
CC   serine O-acetyltransferase. Serine O-acetyltransferase converts
CC   serine to O-acetylserine, that is involved in the formation of cysteine.
CC   This sequence is used as a probe to isolate other plant sulphate
CC   assimilation proteins, for genetic and physical mapping of related genes
CC   and as markers of traits linked to the gene. This is useful for plant
CC   breeding. It is also used to create transgenic plants with altered
CC   levels of serine O-acetyltransferase, or found in cell types or
CC   developmental stages in which they are not normally found.
XX
SQ   Sequence   303 AA;
```

```
  Query Match           50.6%;  Score 831;  DB 21;  Length 303;
  Best Local Similarity   59.0%;  Pred. No. 1.2e-72;
  Matches  160;  Conservative   44;  Mismatches   63;  Indels    4;  Gaps    1;

Qy      44 DDDDVWIKMLEEAKSDVKQEPILSNYYYASITSHRSLESALAHILSVKLSNLNLPSNTLF 103
           |:  || ::  ||: |   || |::: ||:: || ||: :||  |: || :  | |  |:
Db      37 deswvwsqikaearrdadaepalasflyatvlshpsldrslafhlanklcsstllstlly 96

Qy     104 ELFISVLEESPEIIESTKQDLIAVKERDPACISYVHCFLGFKGFLACQAHRIAHTLWKQN 163
```

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          :||:: |   | :  :   ||:| : |||||: : || | :|||||  || |:|| || |:
Db     97 dlfvaslaahptlraavvadllaarsrdpacvgfshcllnykgflaiqaqrvahvlwaqd 156

Qy    164 RKIVALLIQNRVSESFAVDIHPGAKIGKGILLDHATGVVIGETAVVGDNVSILHGVTLGG 223
          |: :|| :|:||:| ||||||| | ||||:|||||||||||||||:|||||||| |||||
Db    157 rralalalqsrvaevfavdihpaaaigkgvlldhatgvvigetavigdnvsilhhvtlgg 216

Qy    224 TGKQSGDRHPKIGDGVLIGAGSCILGNITIGEGAKIGSGSVVVKDVPARTTAVGNPARLI 283
          |||  |||||||||||||||: ||||: || |||||:||:|: ||| ||||||||||:
Db    217 tgkavgdrhpkigdgvligagatilgnvrigagakigagslvlidvpprttavgnparll 276

Qy    284 GGKENPRKHDKIPCLTMDQTSYLTEWSDYVI 314
          |||    | | :|  :|| ||:: :|||| |
Db    277 ggk----kgddmpgesmdhtsfiqqwsdysi 303
```

Search completed: August 21, 2001, 12:07:44
Job time: 91 sec